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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/715,066

11/17/2003

Timothy O'Brien

022438.45514

6392

7590
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01/18/2007

EXAMINER

REDDIG, PETER J

ART UNIT

PAPER NUMBER

1642

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
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3 MONTHS

01/18/2007

PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary

Application No.

10/715,066

Applicant(s)

O'BRIEN ET AL.

Examiner

Peter J. Reddig

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1642

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 17 November 2006.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1, 2 and 21 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1, 2, and 21 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- ☒ Notice of References Cited (PTO-892)
- ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- ☐ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____
- ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- ☐ Notice of Informal Patent Application
- ☒ Other: Appendix 1.

DETAILED ACTION

1. The Amendment filed November 17, 2006 in response to the Office Action of August 7, 2006 is acknowledged and has been entered. Previously pending claims 3-20 have been cancelled, claim 1 has been amended, and new claim 21 has been added.
2. Claims 1, 2, and 21 are currently being examined.
3. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Response to Amendment

4. The declaration under 37 CFR 1.132 filed November 17, 2006 is sufficient to overcome the rejection of claims 1 and 2 based upon O'Brien et al. (Tumor Biology, 2002 May-Jun; 23:154-69, IDS).
5. The following rejections are being maintained:

Double Patenting

6. Claim 2 remains provisionally rejected under 35 USC 101 as claiming the same invention as that of claim 25 of co-pending application 10/475,117.

New Grounds of Rejection

Claim Rejections - 35 USC § 112

7. Claims 1 and 21 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

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The limitation of a polypeptide comprising residues 1-10,427 of SEQ ID NO: 5 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 has no clear support in the specification and the claims as originally filed. Examiner's review of the specification did not reveal support for the newly added limitation. Applicants pointed to support for amended claim 1 in originally filed claims 1, 4, 14, and 15, SEQ ID NO: 1, 4, and 5 and paragraphs 0009, 0011, and 0041. A review of originally filed claims 1, 4, 14, and 15 revealed support for 1) an isolated nucleic acid molecule encoding CA125, 4) the isolated nucleic acid molecule of claim 2 wherein said molecule is a fragment thereof, 14) a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of an one of (a) to (b); and (d) a fragment of any one of (a) to (c), and 15) a purified antibody that selectively binds to an amino acid sequence of the CA125 protein: (a) wherein the amino acid sequence of the CA125 protein comprises the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c). A review of the cited portions of the specification revealed support for SEQ ID NOs: 1-5, the genomic sequence of CA125, a full-length cDNA for CA125, and a CA125 protein, and the domain structure of the CA125 gene and protein. The suggested support is not found persuasive because there is nothing in the specification to suggest the limitation of a polypeptide comprising residues 1-10,427 of SEQ ID NO: 5 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5. Applicant is invited to submit evidence pointing to page

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and line number in the specification wherein support for the newly added limitation can be found.

8. If applicant were able to overcome the rejections set forth above, claims 1 and 21 would still be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, an isolated nucleic acid molecule that encodes a polypeptide **consisting of** residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5, and an isolated nucleic acid molecule encoding CA125, wherein the isolated nucleic acid molecule **consists of** SEQ ID NO: 1 or a fragment thereof, does not reasonably provide enablement for an isolated nucleic acid molecule encoding **a fragment of SEQ ID NO: 5**, wherein the isolated nucleic acid molecule encodes a polypeptide **comprising** residues 1-10,427 **or a fragment of residues 1-10,427** of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 or wherein the isolated nucleic acid molecule **comprises** SEQ ID NO: 1 or a fragment thereof. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are drawn to an isolated nucleic acid molecule encoding a polypeptide comprising a fragment of CA125 (SEQ ID NO: 5), wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

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and line number in the specification wherein support for the newly added limitation can be found.

8. If applicant were able to overcome the rejections set forth above, claims 1 and 21 would still be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, an isolated nucleic acid molecule that encodes a polypeptide **consisting of** residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5, and the isolated nucleic acid molecule encoding CA125, wherein the isolated nucleic acid molecule **consists of** SEQ ID NO: 1 or a fragment thereof, does not reasonably provide enablement for an isolated nucleic acid molecule encoding **a fragment of SEQ ID NO: 5**, wherein the isolated nucleic acid molecule encodes a polypeptide **comprising** residues 1-10,427 **or a fragment of residues 1-10,427** of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 or wherein the isolated nucleic acid molecule **comprises** SEQ ID NO: 1 or a fragment thereof. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The claims are drawn to an isolated nucleic acid molecule encoding a polypeptide comprising a fragment of CA125 (SEQ ID NO: 5), wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

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This means that an antibody that selectively binds SEQ ID NO: 5 can also recognize **any** polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or **any** polypeptide encoded by an isolated nucleic acid molecule comprising SEQ ID NO: 1 or a fragment thereof.

The specification teaches that CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. The specification teaches that elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease, see para. [0003].

The specification teaches that SEQ ID NO: 1 is a DNA sequence showing the 5' upstream region and the amino terminal portion of the CA125 molecule, see 2nd sentence of para. [0009].

The specification teaches that SEQ ID NO: 5 is a CA125 protein and SEQ ID NO: 4 is a full-length cDNA for CA125, see last two lines of para. [0009].

One cannot extrapolate the teachings of the specification to the scope of the claims because polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof contain undefined sequences in addition to those in SEQ ID NO: 5 and one of skill in the art could not predict that an antibody that recognizes and binds CA125 as shown in SEQ ID NO: 5 will recognize and bind the broadly claimed CA125 protein polypeptides comprising fragments of said protein because protein biochemistry is unpredictable and the undefined additional amino acids in a polypeptide comprising residues 1-10,427 of SEQ

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ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof encompassed by the claims would be expected to alter the conformation of the protein and if the antibody binding determinants are not shared by the altered CA125 antigen, the antibodies will not bind.

In particular, protein chemistry is probably one of the most unpredictable areas of biotechnology. For example, Bowie et al (Science, 1990, 257:1306-1310) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function and carry out the instructions of the genome (col 1, p. 1306). Bowie et al further teach that while it is known that many amino acid alterations are possible in any given protein, the position within the protein's sequence where such amino acid alterations can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative alterations or no alterations. However, the specification provides no guidance as to which of the broadly claimed encoded polypeptides comprising CA125 fragments comprise structures or residues that are critical to the binding of antibodies to CA125. The artisan is left to random experimentation in order to determine which of the broadly claimed CA125 proteins will be bound by an antibody that selectively binds to SEQ ID NO: 5. Random experimentation is undue.

Furthermore, the exquisite sensitivity of antibody binding to alterations of even a single amino acid is well known in the art. For example, Coleman et al. (Research in

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Immunology, 1994; 145(1): 33-36) teach single amino acid changes in an antigen can effectively abolish antibody antigen binding. Furthermore, Abaza et al. (Journal of Protein Chemistry, Vol. 11, No. 5, 1992, pages 433-444, see abstract in particular) teach single amino acid substitutions outside the antigenic site on a protein affects antibody binding. These references demonstrate that even a single amino acid alteration or what appears to be an inconsequential chemical modification will often dramatically affect the biological activity and characteristics of a binding protein.

Given the above, and given that the residues of SEQ ID NO: 5 that are critical to binding and recognition by an antibody that selectively binds to SEQ ID NO: 5, or any other antibody, have not been identified, it could not be predicted which protein comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof would be bound by an antibody that selectively binds to SEQ ID NO: 5 and one would not know how to make the claimed invention. Although Applicants might argue that one of ordinary skill could screen for the species that would function as claimed, in particular, screening assays do not enable the claimed invention because the court found in (*Rochester v. Searle*, 358 F.3d 916, Fed Cir., 2004) that screening assays are not sufficient to enable an invention because they are merely a wish or plan for obtaining the claimed chemical invention. Given the exquisite sensitivity of antibodies to changes in the amino acid sequence of the target antigen, it would not be expected and could not be predicted that the invention would function as claimed in the absence of further guidance. Given the teaching of Bowie et al that the amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-

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dimensional structures that allows them to function and carry out the instructions of the genome, it is clear that the folding and shape of the undefined polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof cannot be predicted. The specification provides neither information nor guidance on how to predictably identify which of the broadly claimed polypeptides comprising residues 1-10,427 of SEQ ID NO: 5 or fragments thereof or the polypeptides encoded by nucleic acids that comprise SEQ ID NO: 1 or fragments thereof will be bound by an antibody that selectively binds to SEQ ID: 5.

The specification provides insufficient guidance with regard to these issues and provides no working examples which would provide guidance to one skilled in the art and no evidence has been provided which would allow one of skill in the art to predict that the invention would function as broadly claimed with a reasonable expectation of success. For the above reasons, it appears that undue experimentation would be required to practice the claimed invention.

9. Claims 1 and 21 are rejected under 35 USC 112, first paragraph, as lacking an adequate written description in the specification.

The claims are drawn to an isolated nucleic acid molecule encoding CA125 (SEQ ID NO: 5) or a fragment thereof, wherein the isolated nucleic acid molecule encodes a polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 recognized by an antibody that selectively binds to SEQ ID NO: 5 and wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof.

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Although drawn to DNA arts, the findings in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) and Enzo Biochem, Inc. V. Gen-Probe Inc. are relevant to the instant claims. The Federal Circuit addressed the application of the written description requirement to DNA-related inventions in University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997). The court stated that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." *Id.* At 1567, 43 USPQ2d at 1405. The court also stated that

a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA" without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

Id. At 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." *Id.*

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." *Id.*

The Federal Circuit has recently clarified that a DNA molecule can be adequately described without disclosing its complete structure. See Enzo Biochem, Inc. V. Gen-Probe Inc., 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). The Enzo court adopted the standard that "the written description requirement can be met by 'show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics.... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. " Id. At 1324, 63 USPQ2d at 1613 (emphasis omitted, bracketed material in original).

The inventions at issue in Lilly and Enzo were DNA constructs per se, the holdings of those cases are also applicable to claims such as those at issue here.

Thus, the instant specification may provide an adequate written description of an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 per Lilly by structurally describing a representative number of isolated nucleic acid molecules encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 or by describing "structural features common to the members of the genus, which features constitute a substantial portion of the genus." Alternatively, per Enzo, the specification can show that the claimed invention is complete "by disclosure of sufficiently detailed, relevant identifying

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characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics."

In this case, the specification does not describe an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 in a manner that satisfies either the Lilly or Enzo standards. The specification does not provide the complete structure of any isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5, nor does the specification provide any partial structure of such isolated nucleic acid, nor any physical or chemical characteristics of the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 nor any functional characteristics coupled with a known or disclosed correlation between structure and function other than SEQ ID NOS: 1 and 4. Although the specification discloses SEQ ID NOS: 1 and 4, this does not provide a description of an isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 the standard set out in Enzo.

The specification also fails to describe the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 by the test set out in Lilly. The specification describes only SEQ ID NOs: 1 and 4. Therefore, it necessarily fails to describe a "representative number" of such species. In addition, the specification also does not describe "structural features common to the members of the genus, which features constitute a substantial portion of the genus.

Thus, the specification does not provide an adequate written description of the isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof recognized by an antibody that selectively binds to SEQ ID NO: 5 that is required to practice the claimed invention.

Some of the arguments drawn to the previous rejection of claims 3 and 4 are relevant to the instant rejection. In regards to claim 1 and the written description requirement Applicants argue that the complete structure of "An isolated nucleic acid molecule encoding CA 125 (SEQ ID NO: 5) or a fragment thereof" is disclosed in the specification and recited in claim 1.

Applicants argue that the complete structures of genomic nucleic acid sequences encoding SEQ ID NO: 5 and fragments thereof are disclosed in the specification in SEQ ID NOS: 1-3.

Applicants argue that the complete structure of a cDNA encoding SEQ ID NO: 5 is disclosed as SEQ ID NO: 4. Applicants argue that the complete structure of any other nucleic acid encoding SEQ ID NO: 5 or a fragment thereof is disclosed by the disclosure of SEQ ID NO: 5 in the

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specification and by the knowledge of the genetic code. Applicants argue that the complete and exact structure of every possible species within the genus claimed by claim 1 is disclosed in the specification.

In regards to University of California v. Eli Lilly and Co., 119 F.3d 1559, 43 USPQ2d 1398 (Fed. Cir. 1997) Applicants argue that the claims 1 and 2 recite the precise structure of CA125 (SEQ ID NO: 5). Applicant argues that this also, with knowledge of the genetic code, inherently discloses the structure of every nucleic acid encoding SEQ ID NO: 5 or a fragment thereof.

Applicants' arguments have been carefully considered, but have not been found persuasive because applicant is arguing limitations not recited in the claims as currently constituted. The comprising language of claim 1 does not limit claim to sequences contained only in SEQ ID NO: 4 or 5, rather claim 1 encompasses any isolated nucleic acid molecule encoding a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 or wherein the isolated nucleic acid molecule comprises SEQ ID NO: 1 or a fragment thereof encoding a polypeptide recognized by an antibody that selectively binds to SEQ ID NO: 5. Thus, numerous unknown and undefined amino acid additions to a CA125 polypeptide comprising residues 1-10,427 or a fragment of residues 1-10,427 of SEQ ID NO: 5 and polypeptides encoded by nucleic acids comprising SEQ ID NO: 1 or fragments thereof are encompassed by the claims and for the reasons set forth above, neither the specification nor the claims as originally filed meet the written description requirements of 35 USC 112, first paragraph.

Claim Rejections - 35 USC § 102

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10. Claim 1 and 21 are rejected under 35 U.S.C. 102(b) as being anticipated by DOE Joint Genome Institute, Homo sapiens chromosome 19 clone CTD-2596O15, LOW-PASS SEQUENCE SAMPLING, Accession No. AC016584, Version AC016584.2, GI 6758722, January 26, 2000 as evidenced by Appendix 1.

The DOE Joint Genome Institute teaches nucleotide sequences that are homologous to CA125 nucleic acids that encode fragments of residues 1-10,427 of SEQ ID NO: 5.

Although the reference does not specifically state that the nucleic acid sequences are a CA125 sequence and that an antibody that selectively binds to SEQ ID NO: 5 will recognize the protein encoded by the nucleic acid of Accession No. AC016584, Version AC016584.2, the claimed product appears to be the same as the prior art product, absent a showing of unobvious differences. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from that taught by the prior art and to establish patentable differences. See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977).

11. All other objections and rejections recited in the Office Action of August 7, 2006 are withdrawn.

12. No claims allowed.

13. This action is a **final rejection** and is intended to close the prosecution of this application. Applicant's reply under 37 CFR 1.113 to this action is limited either to an appeal to

the Board of Patent Appeals and Interferences or to an amendment complying with the requirements set forth below.

If applicant should desire to appeal any rejection made by the examiner, a Notice of Appeal must be filed within the period for reply identifying the rejected claim or claims appealed. The Notice of Appeal must be accompanied by the required appeal fee.

If applicant should desire to file an amendment, entry of a proposed amendment after final rejection cannot be made as a matter of right unless it merely cancels claims or complies with a formal requirement made earlier. Amendments touching the merits of the application which otherwise might not be proper may be admitted upon a showing a good and sufficient reasons why they are necessary and why they were not presented earlier.

A reply under 37 CFR 1.113 to a final rejection must include the appeal from, or cancellation of, each rejected claim. The filing of an amendment after final rejection, whether or not it is entered, does not stop the running of the statutory period for reply to the final rejection unless the examiner holds the claims to be in condition for allowance. Accordingly, if a Notice of Appeal has not been filed properly within the period for reply, or any extension of this period obtained under either 37 CFR 1.136(a) or (b), the application will become abandoned.

14. Applicants' amendment necessitated the new grounds of rejection. Thus, **THIS ACTION IS MADE FINAL**. Applicant is reminded of the extension of time policy as set forth in 37 C.F.R. ' 1.136(a).

A SHORTENED STATUTORY PERIOD FOR RESPONSE TO THIS FINAL ACTION IS SET TO EXPIRE THREE MONTHS FROM THE DATE OF THIS ACTION. IN THE EVENT A FIRST RESPONSE IS FILED WITHIN TWO MONTHS OF THE MAILING DATE

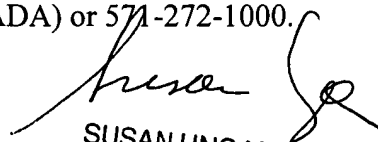
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OF THIS FINAL ACTION AND THE ADVISORY ACTION IS NOT MAILED UNTIL AFTER THE END OF THE THREE-MONTH SHORTENED STATUTORY PERIOD, THEN THE SHORTENED STATUTORY PERIOD WILL EXPIRE ON THE DATE THE ADVISORY ACTION IS MAILED, AND ANY EXTENSION FEE PURSUANT TO 37 C.F.R. ' 1.136(a) WILL BE CALCULATED FROM THE MAILING DATE OF THE ADVISORY ACTION. IN NO EVENT WILL THE STATUTORY PERIOD FOR RESPONSE EXPIRE LATER THAN SIX MONTHS FROM THE DATE OF THIS FINAL ACTION.

15. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Peter J. Reddig whose telephone number is (571) 272-9031. The examiner can normally be reached on M-F 8:30 a.m.-5:00 p.m..

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Shanon Foley can be reached on (571) 272-0890. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.


SUSAN UNGAR, PH.D
PRIMARY EXAMINER

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Signature on previous page

Peter J. Reddig, Ph.D.
Examiner
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PJR

SCORE Search Results Details for Application 10715066 and Search Result 20060605_161408_us- 10-715-066-4_copy_500_1000.rge.

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OM nucleic - nucleic search, using sw model

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Title: US-10-715-066-4_COPY_500_1000
Perfect score: 501
Sequence: 1 aaagaaccagcccatcgctg.....aaccactggatatcccttct 501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
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8: gb_sy:*
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10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db	500	AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAACTCCCTCTAGGAACTACCCTG	559
Qy	61	CTACAAGCATGGTTTCAGGATTGAGTTCCCCAAGGACCAGGACCAGTTCCACAGAAGGAA	120
Db	560	CTACAAGCATGGTTTCAGGATTGAGTTCCCCAAGGACCAGGACCAGTTCCACAGAAGGAA	619
Qy	121	ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCCAGTCA	180
Db	620	ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCCAGTCA	679
Qy	181	CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAACTGAAGGTGACAGCACAGAGACCC	240
Db	680	CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAACTGAAGGTGACAGCACAGAGACCC	739
Qy	241	CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAAACATTTGCAGATT	300
Db	740	CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAAACATTTGCAGATT	799
Qy	301	CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG	360
Db	800	CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG	859
Qy	361	ACTCACATACTCCAGGAAGGACAAACCCATCATTGGGACACTTTATTCTTCCTTCCTTG	420
Db	860	ACTCACATACTCCAGGAAGGACAAACCCATCATTGGGACACTTTATTCTTCCTTCCTTG	919
Qy	421	ACCTATCACCTAAAGGGACCCCAAATTCCAGAGGTGAAACAAGCCTGGAAGTATTCTAT	480
Db	920	ACCTATCACCTAAAGGGACCCCAAATTCCAGAGGTGAAACAAGCCTGGAAGTATTCTAT	979
Qy	481	CAACCACTGGATATCCCTTCT	501
Db	980	CAACCACTGGATATCCCTTCT	1000

RESULT 5

AC016584/c

LOCUS AC016584 132457 bp DNA linear PRI 29-MAY-2002

DEFINITION Homo sapiens chromosome 19 clone CTD-2596015, complete sequence.

ACCESSION AC016584

VERSION AC016584.5 GI:21240686

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 132457)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On May 29, 2002 this sequence version replaced gi:12965319.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.7% of Sequence;

Estimated Total Number of Errors is 0.3.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 138.1kb). It is clipped at the overlap with AC011464.

The number of bases overlapped is 14325.

FEATURES
source 1. .132457
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2596015"

ORIGIN

Query Match 100.0%; Score 501; DB 5; Length 132457;
Best Local Similarity 100.0%; Pred. No. 2.8e-161;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAACCTCCTCTAGGAACTACCTG 60
|||||
Db 29314 AAAGAACCAGCCCATCGCTGAGTCCCAGGTCAATGGAACCTCCTCTAGGAACTACCTG 29255

Qy 61 CTACAAGCATGGTTTCAGGATTGAGTCCCAAGGACCAGGACCAGTTCACAGAAGGAA 120
|||||
Db 29254 CTACAAGCATGGTTTCAGGATTGAGTCCCAAGGACCAGGACCAGTTCACAGAAGGAA 29195

Qy 121 ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCAGTCA 180
|||||
Db 29194 ATTTTACCAAAGAAGCATCTACATACACACTCACTGTAGAGACCACAAGTGGCCAGTCA 29135

Qy 181 CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAGTGAAGGTGACAGCACAGAGACCC 240
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Db 29134 CTGAGAAGTACACAGTCCCCACTGAGACCTCAACAAGTGAAGGTGACAGCACAGAGACCC 29075

Qy 241 CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAACATTTGCAGATT 300
|||||
Db 29074 CCTGGGACACAAGATATATTCCTGTAAAAATCACATCTCCAATGAAAACATTTGCAGATT 29015

Qy 301 CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG 360
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Db 29014 CAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGACTCCAGCTGAGACCACAGTTACTG 28955

Qy 361 ACTCACATACTCCAGGAAGGACAAACCCATCATTTGGGACACTTTATTCTTCCTTCCTTG 420
|||||
Db 28954 ACTCACATACTCCAGGAAGGACAAACCCATCATTTGGGACACTTTATTCTTCCTTCCTTG 28895

Qy 421 ACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGAAACAAGCCTGGAAGTATTCTAT 480
|||||
Db 28894 ACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGAAACAAGCCTGGAAGTATTCTAT 28835

Qy 481 CAACCACTGGATATCCCTTCT 501
|||||
Db 28834 CAACCACTGGATATCCCTTCT 28814

RESULT 6

AC166942

LOCUS AC166942 247108 bp DNA linear HTG 23-JAN-2006

DEFINITION Bos taurus clone CH240-121L8, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.

ACCESSION AC166942

VERSION AC166942.2 GI:85665651

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 247108)
AUTHORS Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A.,
Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De
Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,

[start](#) | [next page](#)

SCORE 1.3 BuildDate: 11/17/2006



Sequence Revision History

[PubMed](#)[Nucleotide](#)[Protein](#)[Genome](#)[Structure](#)[PMC](#)[Taxonomy](#)[OMIM](#)[Books](#)

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Revision history for AC016584

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Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

GI	Version	Update Date	Status	I	II
21240686	5	May 29 2002 7:29 AM	Live	<input checked="" type="radio"/>	<input type="radio"/>
12965319	4	Feb 20 2001 4:55 AM	Dead	<input type="radio"/>	<input checked="" type="radio"/>
9211207	3	Jul 15 2000 4:53 AM	Dead	<input type="radio"/>	<input type="radio"/>
6758722	2	Mar 3 2000 5:46 PM	Dead	<input type="radio"/>	<input type="radio"/>
6758722	2	Jan 26 2000 6:08 PM	Dead	<input type="radio"/>	<input type="radio"/>
6524122	1	Dec 4 1999 6:04 PM	Dead	<input type="radio"/>	<input type="radio"/>

Accession AC016584 was first seen at NCBI on Dec 4 1999 6:04 PM

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Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

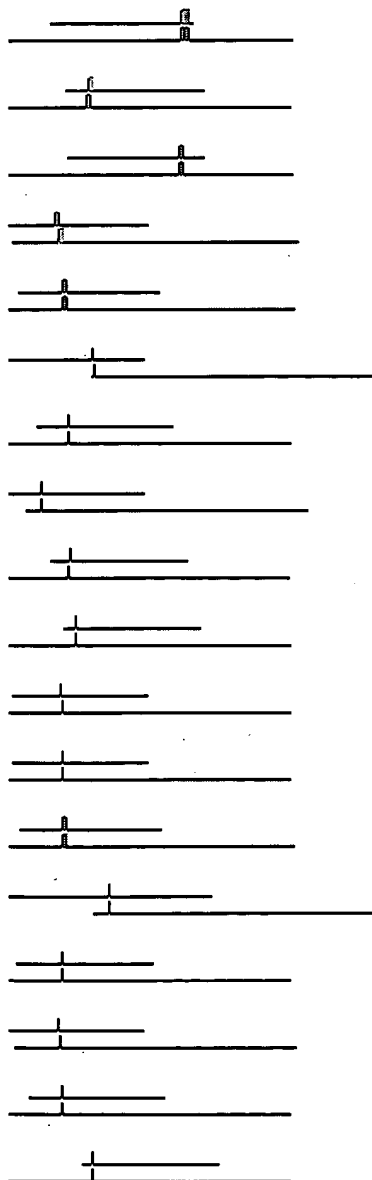
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.15 [Oct-15-2006]

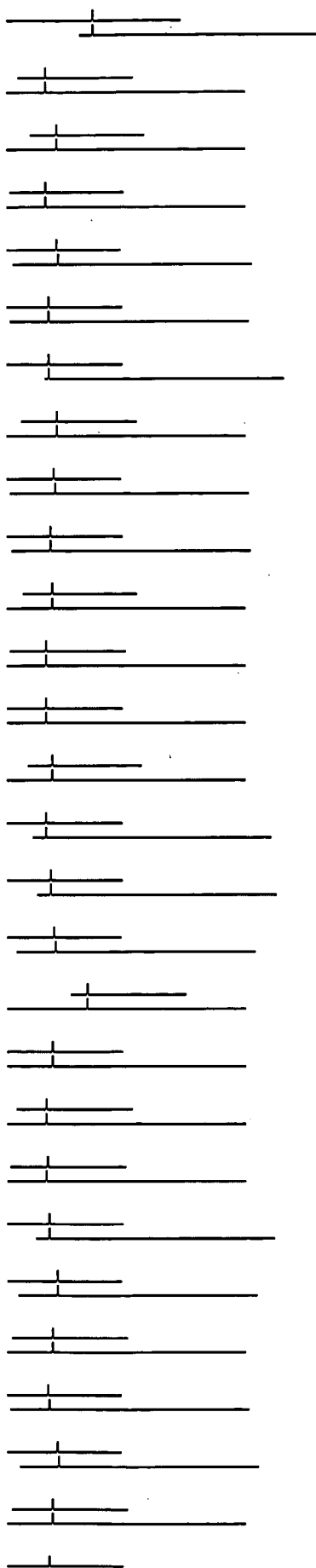
Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ View option Masking character option Masking color option ☐ Show CDS translation **Sequence 1:** gi|24419040|gb|AF414442.2| = *SEQ ID NO: 4*

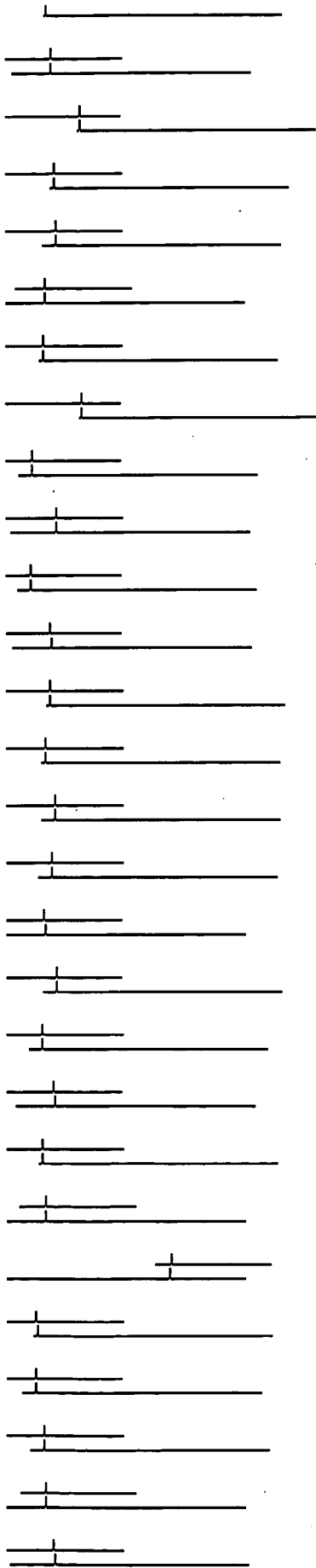
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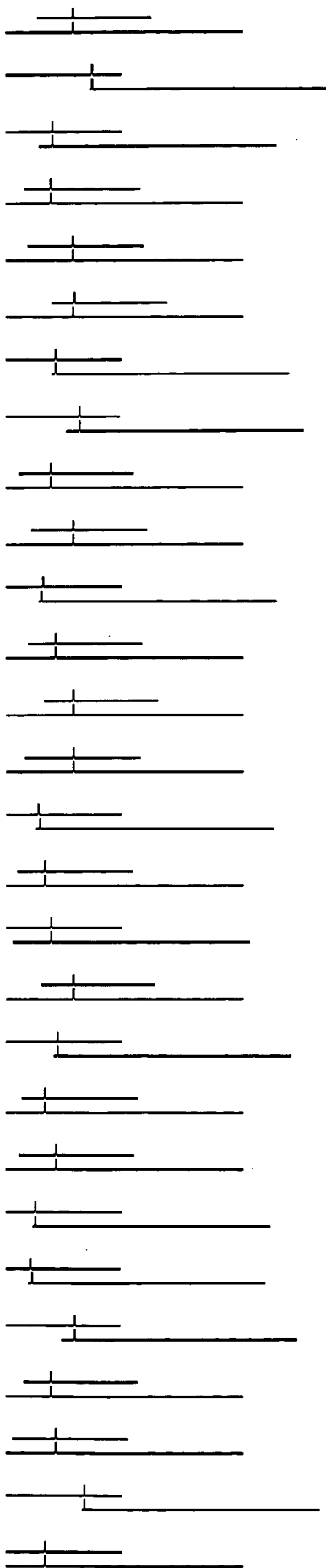
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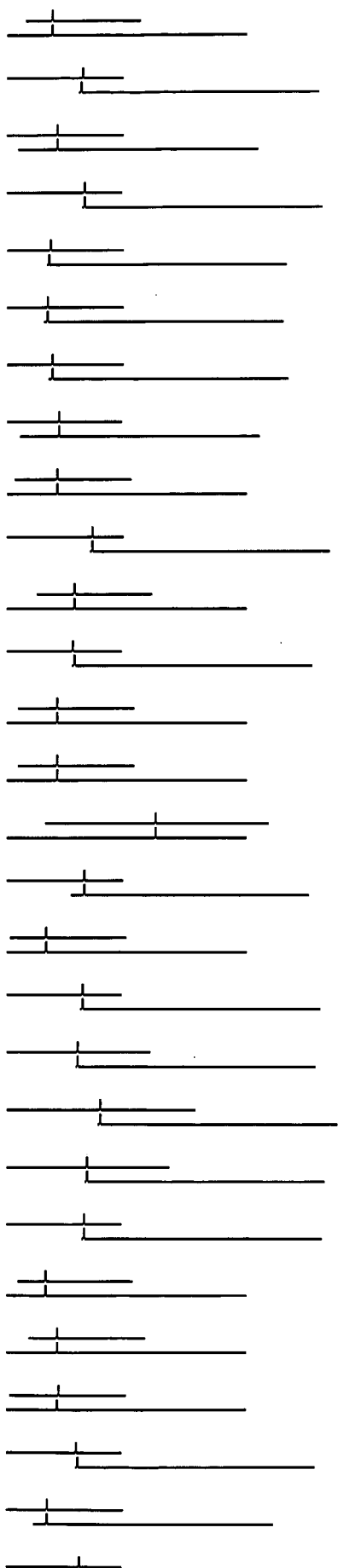
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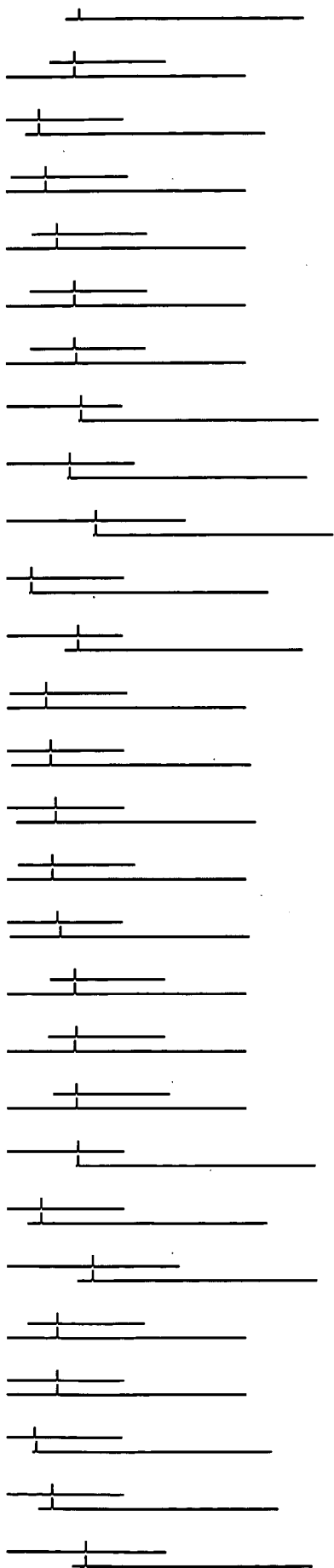












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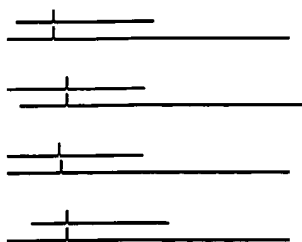
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NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

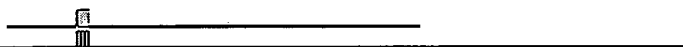


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Identities = 1935/1937 (99%), Gaps = 2/1937 (0%)
Strand=Plus/Minus

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Sbjct	86743	CAGGACCAGTTCCACAGAAGGAA-TTTTACCAAAGAAGCATCTACATACACACTCACTGT	86685
Query	657	AGAGACCACAAGTGGCCCACTGAGAGTACACAGTCCCCACTGAGACCTCAACAAC	716
Sbjct	86684	AGAGACCACAAGTGGCCCACTGAGAGTACACAGTCCCCACTGAGACCTCAACAAC	86625
Query	717	TGAAGGTGACAGCACAGAGACCCCCTGGGACACAAGATATATTCCTGTAAAAATCACATC	776
Sbjct	86624	TGAAGGTGACAGCACAGAGACCCCCTGGGACACAAGATATATTCCTGTAAAAATCACATC	86565
Query	777	TCCAATGAAAACATTTGCAGATTCAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGAC	836
Sbjct	86564	TCCAATGAAAACATTTGCAGATTCAACTGCATCCAAGGAAAATGCCCCAGTGTCTATGAC	86505
Query	837	TCCAGCTGAGACCACAGTTACTGACTCACATACTCCAGGAAGGACAAACCCATCATTGG	896
Sbjct	86504	TCCAGCTGAGACCACAGTTACTGACTCACATACTCCAGGAAGGACAAACCCATCATTGG	86445
Query	897	GACACTTTATTCTTCCTTCCTTGACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGA	956
Sbjct	86444	GACACTTTATTCTTCCTTCCTTGACCTATCACCTAAAGGGACCCCAAATTCAGAGGTGA	86385
Query	957	AACAAGCCTGGAAGTATTCTATCAACCACTGGATATCCCTTCTCCTCTCCTGAACCTGG	1016
Sbjct	86384	AACAAGCCTGGAAGTATTCTATCAACCACTGGATATCCCTTCTCCTCTCCTGAACCTGG	86325
Query	1017	CTCTGCAGGACACAGCAGAATAAGTACCAGTGCGCCTTTGTGTCATCATCTGCTTCAGTTCT	1076
Sbjct	86324	CTCTGCAGGACACAGCAGAATAAGTACCAGTGCGCCTTTGTGTCATCATCTGCTTCAGTTCT	86265
Query	1077	CGATAATAAAATATCAGAGACCAGCATATTCTCAGGCCAGAGTCTCACCTCCCCTCTGTC	1136
Sbjct	86264	CGATAATAAAATATCAGAGACCAGCATATTCTCAGGCCAGAGTCTCACCTCCCCTCTGTC	86205
Query	1137	TCCTGGGGTGCCCCGAGGCCAGAGCCAGCACAATGCCCAAAGTCTCAGCTATCCCTTTTCCAT	1196
Sbjct	86204	TCCTGGGGTGCCCCGAGGCCAGAGCCAGCACAATGCCCAAAGTCTCAGCTATCCCTTTTCCAT	86145
Query	1197	GACACTAAGCAATGCAGAAACAAGTGCCGAAAGGGTCAGAAGCACAATTCCTCTCTGGG	1256

Sbjct	86144	 GACACTAAGCAATGCAGAAACAAGTGCCGAAAGGGTCAGAAGCACAAATTTCTCTCTGGG	86085
Query	1257	GACTCCATCAATATCCACAAAGCAGACAGCAGAGACTATCCTTACCTTCCATGCCTTCGC	1316
Sbjct	86084	 GACTCCATCAATATCCACAAAGCAGACAGCAGAGACTATCCTTACCTTCCATGCCTTCGC	86025
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Sbjct	86024	 TGAGACCATGGATATACCCAGCACCCACATAGCCAAGACTT-GGCTTCAGAATGGTTGGG	85966
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Query	1437	CACTTTAGTCTCAGAGGAGACCAACACCCATCACTCCACGAGTGGAAGGAAACAGAAGG	1496
Sbjct	85905	 CACTTTAGTCTCAGAGGAGACCAACACCCATCACTCCACGAGTGGAAGGAAACAGAAGG	85846
Query	1497	AACTTTGAATACATCTATGACTCCACTTGAGACCTCTGCTCCTGGAGAAGAGTCCGAAAT	1556
Sbjct	85845	 AACTTTGAATACATCTATGACTCCACTTGAGACCTCTGCTCCTGGAGAAGAGTCCGAAAT	85786
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Query	1797	CCAGCACACACAGTGGGTGGAGACAAGTCCTAGCATGAAAACAGAGAGACCCCCAGCATC	1856
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Query	1977	CGGAGAATCCACAGCTGGCCCAACCACCCATCAGTTTGCTGTTCCCACTGGGATTTCAAT	2036
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Sbjct	85305	 GACAGGAGGCAGCAGCACCAGGGGAAGCCAGGGCACAACCCACCTACTCACCAGAGCCAC	85246
Query	2097	AGCATCATCTGAGACATCCGAGATTTGACTCTGGCCACGAACGGTGTCCAGTCTCCGT	2156
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Sbjct	85185	 GTCTCCAGCAGTGAGCAAGACGGCTGCTGGCTCAAGTCCTCCAGGAGGGACAAAGCCATC	85126

Query	2217	ATATACAATGGTTTCTTCTGTCCCTGAGACATCATCTCTACAGTCCTCAGCTTTCAG	2276
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Sbjct	85065	GGAAGGAACCAGCCTGGGACTGACTCCATTAAACACTAGACATCCCTTCTTCCCCTGA	85006
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Sbjct	85005	ACCAGACTCTGCAGGACACACCAAGATAAGCACCAGCATTCTCTGTTGTCATCTGCTTC	84946
Query	2397	AGTTCTTGAGGATAAAGTGTGAGCGACCAGCACATTCTCACACCACAAAGCCACCTCATC	2456
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Sbjct	84885	TATTACCACAGGGACTCCTGAAATCTCAACAAAGACAAAGCCCAGCTCAGCCGTTCTTTC	84826
Query	2517	CTCCATGACCCTAAGCA	2533
Sbjct	84825	CTCCATGACCCTAAGCA	84809



Score = 2488 bits (1294), Expect = 0.0
 Identities = 1347/1361 (98%), Gaps = 5/1361 (0%)
 Strand=Plus/Plus

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Sbjct	38817	CACTCAGCTTCCCACCACCACTTCTGCACATCCAGAGCAGGTGCCAGATCAGCAGCAAC	38876
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Sbjct	38877	AACTCTGGATGTGATCCACACACAGCAAAACTCCAGATGCAACTTTTCAGAGACAAGG	38936
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Sbjct	38937	GCAGACAGCTCTTACAACAGAGGCAAGAGCTACATCTGACTCCTGGAATGAGAAAGAAAA	38996
Query	11829	ATCAACCCCAAGTGCACCTTGGATCACTGAGATGATGAATTCTGTCTCAGAAGATACCAT	11888
Sbjct	38997	ATCAACCCCAAGTGCACCTTGGATCACTGAGATGATGAATTCTGTCTCAGAAGATACCAT	39056
Query	11889	CAAGGAGGTTACCAGCTCCTCCAGTGTATTAAAGGACCCTGAATACGCTGGACATAAACT	11948
Sbjct	39057	CAAGGAGGTTACCAGCTCCTCCAGTGTGTTAA-GGACCCTGAATACGCTGGACATAAACT	39115
Query	11949	TGGAATCTGGGACGACTTCATCCCCAAGTTTGGAAGAGCAGCCCATATGAGAGAGTTGCC	12008
Sbjct	39116	TGGAATCTGGGACGACTTCATCCCCAAGTT-GGAAAGAGCAGCCCATATGAGAGAATTGCC	39174
Query	12009	CCTTCTGAGTCCACCACAGGACAAAGAGGCAATTCACCCTTCTACAAACACAGTAGAGAC	12068
Sbjct	39175	CCTTCTGAGTCTACCACAG-ACAAAGAGGCAATTCACCCTTCTACAAACACAGTAGAGAC	39233

Score = 2207 bits (1148), Expect = 0.0
Identities = 1194/1210 (98%), Gaps = 5/1210 (0%)
Strand=Plus/Minus

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Query	10393	ACCACAGCCATTCCCTCCACTGTCCTGAATAATAAGATAATGGCAGCTGAACAACAGACA	10452
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Query	10453	AGTCGATCTGTGGATGAGGCTTATTTCATCAACTAGTTCTTGGTCAGATCAGACATCTGGG	10512
Sbjct	84660	AGTCGATCTGTGGATGAGGCTTATTTCATCAACTAGTTCTTGGTCAGATCAGACATCTGGG	84601
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Query	10573	GCACAAACCACCTCACTAGTGTCTCTGCCCTCTGGAGACCAAGGCATTACAAGCCTCACC	10632
Sbjct	84540	GCACAAACCACCTCACTAGTATCTCTGCCCTCTGGAGACCAAGGCATTACAAGCCTCACC	84481
Query	10633	AATCCCTCAGGAGGAAAAACAAGCTCTGCGTCATCTGTACATCTCCTTCAATAGGGCTT	10692
Sbjct	84480	AATCCCTCAGGAGGAAAAACAAGCTCTGCGTCATCTGTACATCTCCTTCAATAGGGCTT	84421
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Sbjct	84420	GAGACTCTGATGGCCAATGTAAGTGCAGTGACAAGTGACATTGCCCTACTGCTGGGCAT	84361
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Sbjct	84360	CTATCTCAGACTTCATCTCCTGCGGAAGTGAGCATCCTGGACATAACCACAGCTCCTACT	84301
Query	10813	CCAGGTATCTCCACCACCATCACCACCATGGGAACCAACTCAATCTCAACTACCACACCC	10872
Sbjct	84300	CCAGGTATCTCCACCACCATCACCACCATGGGAACCAACTCAATCTCAACTACCACACCC	84241
Query	10873	AACCCAGAAGTGGGTATGAGTACCATGGACAGCACCCCGGCCACAGAGAGGCGCACAACT	10932
Sbjct	84240	AACCCAGAAGTGGGTATGAGTACCATGGACAGCACCCCGGCCACAGAGAGGCGCACAACT	84181
Query	10933	TCTACAGAACACCCTTCCACCTGGTCTTCCACAGCTGCATCAGATTCCTGGACTGTCACA	10992
Sbjct	84180	TCTACAGAACACCCTTCCACCTGGTCTTCCACAGCTGCATCAGATTCCTGGACTGTCACA	84121
Query	10993	GACATGACTTCAAACCTTGAAAGTTGCAAGATCTCCTGGAACAATTTCCACAATGCATACA	11052
Sbjct	84120	GACATGACTTCAAACCTTGAAAGTTGCAAGATCTCCTGGAACAATTTCCACAATGCATACA	84061
Query	11053	ACTTCATTCTTAGCCTCAAGCACTGAATTAGACTCCATGTCTACTCCCCATGGCCGTATA	11112
Sbjct	84060	ACTTCATTCTTAGCCTCAAGCACTGAATTAGACTCCATGTCTACTCCCCATGGCCGTATA	84001
Query	11113	ACTGTCATTGGAACCAGCCTGGTCACTCCATCCTCTGATGCTTCAGCTGTAAAGACAGAG	11172
Sbjct	84000	ACTGTCATTGGAACCAGCCTGGTCACTCCATCCTCTGATGCTTCAGCTGTAAAGACAGAG	83941
Query	11173	ACCAGTACAAGTGAAAGAACATTGAGTCCTTCAGACACAACCTGCATCTACTCCCATCTCA	11232
Sbjct	83940	ACCAGTACAAGTGAAAGAACATTGAGTCCTTCAGACACAACCTGCATCTACTCCCATCTCA	83881
Query	11233	ACTTTTTCTCGTGTCCAGAGGATGAGCATCTCAGTTCCTGACATTTTAAGTACAAGTTGG	11292

Sbjct	83880		ACTTTTTCTCGTGTCAGAGGATGAGCATCTCAGTTCCTGACATTTTAAGTACAAGTTGG	83821
Query	11293		ACTCCAGTAGTACAGAAGCAGAAGATGTGCCTGTTTCAATGGTTTCTACAGATCATGCT	11352
Sbjct	83820		ACTCCAGTAGTACAGAAGCAGAAGATGTGCCTGTTTCAATGGTTTCTACAGATCATGCT	83761
Query	11353		AGTACAAAGACTGACCCAAATACGCCCTGTCCACTTTTCTGTTTGATTCTCTGT---CC	11409
Sbjct	83760		AGTACAAAGACTGACCCAAATATGCCCTGTCCACTTTTCTGTTTGATTCTCTGTTCANC	83701
Query	11410		ACTCTTG-AC-TGGGACACTGGGAGATCTCTGTATCAGCCACAGCCACTACCTCAGCTC	11467
Sbjct	83700		ACTCTTGATACATGGGACACTGGGAGATCTCTGTATCAGCCACAGCCACTACCTCAGCTC	83641
Query	11468		CTCAGGGGGCCACAACCTCCCAAGAACTCACTTTGGAAACCATGATCAGCCAGCTACCT	11527
Sbjct	83640		CTCAGGGGGCCACAACCTCCCAAGAACTCACTTTGGAAACCATGATCAGCCAGCTACCT	83581
Query	11528		CACAGTTGCC	11537
Sbjct	83580		CACAGTTGCC	83571

Score = 1302 bits (677), Expect = 0.0
Identities = 728/739 (98%), Gaps = 3/739 (0%)
Strand=Plus/Plus

Query	23289		ACCTGCCGTGACCTCACCTCATCTGTTCACCACATTCTAGCACATATnnnnnnnTC	23348
Sbjct	22545		ACCTGCCGTGACCTCACCTCATCTGTTCACCACATTCTAGCACATATCCCCCCTC	22603
Query	23349		TCCCCTTCTGTGACTTCACTTCTCACCTCTGGCCCGGCGACAACCACAGATATCTTGGG	23408
Sbjct	22604		TCCCCTTCTGTGACTTCACTTCTCACCTCTGGCCCGGCGACAACCACAGATATCTTGGG	22663
Query	23409		TACAAGCACAGAACCTGGAACCACTTCACTTCAAGTTTGAGCACCACCTCCCATGAGAG	23468
Sbjct	22664		TACAAGCACAGAACCTGGAACCACTTCACTTCAAGTTTGAGCACCACCTCCCATGAGAG	22723
Query	23469		ACTGACCACTTACAAAGACACTGCACATACAGAAGCCGTGCATCCTTCCACAAACACAGG	23528
Sbjct	22724		ACTGACCACTTACAAAGACACTGCACATACAGAAGCCGTGCATCCTTCCACAAACACAGG	22783
Query	23529		AGGGACCAATGTGGCAACCACAGCTCTGGATATAAATCACAGTCCTCTGTCTAGCTGA	23588
Sbjct	22784		AGGGACCAATGTGGCAACCACAGCTCTGGATATAAATCACAGTCCTCTGTCTAGCTGA	22843
Query	23589		CTCATCTCCAATGTGTACCACCTCCACCATGGGGGATACAAGTGTTCTCACATCAACTCC	23648
Sbjct	22844		CTCATCTCCAATGTGTACCACCTCCACCATGGGGGATACAAGTGTTCTCACATCAACTCC	22903
Query	23649		TGCCTTCCTTGAGACTAGGAGGATTAGACAGAGCTAGCTTCCTCCCTGACCCCTGGATT	23708
Sbjct	22904		TGCCTTCCTTGAGACTAGGAGGATTAGACAGAGCTAGCTTCCTCCCTGACCCCTGGATT	22963
Query	23709		GAGGGAGTCCAGTGGCTCTGAAGGGACCAGCTCAGGCACCAAGATGAGCACTGTCTCTC	23768
Sbjct	22964		GAGGGAGTCCAGTGGCTCTGAAGGGACCAGCTCAGGCACCAAGATGAGCACTGTCTCTC	23023
Query	23769		TAAAGTGCCCACTGGTGCTACTACTGAGATCTCAAGGAAGACGTCACCTCCATCCCAGG	23828

Sbjct	23024	 TAAAGTGCCCACTGGTGCTACTACTGAGATCTCCAAGGAAGACGTACCTCCATCCCAGG	23083
Query	23829	TCCCGCTCAATCCACAATATCACCAGACATCTCCACAAGAACCGTCAGCTGGTTCTCTAC	23888
Sbjct	23084	 TCCCGCTCAATCCACAATATCACCAGACATCTCCACAAGAACCGTCAGCTGGTTCTCTAC	23143
Query	23889	ATCCCCTGTCATGACAGAATCAGCAGAAATAACCATGAACACCCATACAAGTCCTTTAGG	23948
Sbjct	23144	 ATCCCCTGTCATGACAGAATCAGCAGAAATAACCATGAACACCCATACAAGTCCTTTAGG	23203
Query	23949	GGCCACAACACAAGGCACCACTACTTT-GGCCACGTCAAGCACAACCTCTTTGACAATGA	24007
Sbjct	23204	 GGCCACAACACAAGGCACCACTACTTTGGGCCACGTCAAGGCACAACCTCTTTGACAATGA	23263
Query	24008	CACA-CTCAACTATATCTC 24025	
Sbjct	23264	 CACACCTCCACTATATCTC 23282	

Score = 1190 bits (619), Expect = 0.0
Identities = 639/644 (99%), Gaps = 2/644 (0%)
Strand=Plus/Plus

Query	21620	CCACAGACATGTTACACACAAGCCCAGAACTTGTAACCAGTTCACCTCCAAAGCTGAGCC	21679
Sbjct	26180	 CCACAGACATGTTACACACAAGCCCAGAACT-GTAACCAGT-CACCTCCAAAGCTGAGCC	26237
Query	21680	ACACTTCAGATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	21739
Sbjct	26238	 ACACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	26297
Query	21740	CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTTTGGACATGAATCCCCTT	21799
Sbjct	26298	 CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCCCCTT	26357
Query	21800	CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCA	21859
Sbjct	26358	 CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCA	26417
Query	21860	CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	21919
Sbjct	26418	 CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	26477
Query	21920	AGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	21979
Sbjct	26478	 AGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	26537
Query	21980	CAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCCATTGGTGCTACTACTG	22039
Sbjct	26538	 CAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCCGTTGGTGCTACTACTG	26597
Query	22040	AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	22099
Sbjct	26598	 AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	26657
Query	22100	CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAAGTTCCTACTTCCCCCA	22159
Sbjct	26658	 CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAAGTTCCTACTTCCCCCA	26717
Query	22160	TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	22219

Sbjct	26718		TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	26777
Query	22220		CAGAGAGTACCTTTACATTAGACACATCAACCACTCCCTCCTTG	22263
Sbjct	26778		CAGAGAGTACCTTTACATTAGACACATCAACCACTCCCTCCTTG	26821

Score = 775 bits (403), Expect = 0.0
 Identities = 536/560 (95%), Gaps = 18/560 (3%)
 Strand=Plus/Minus

Query	24772		ACCTCCAGCATAATGACAGAATCAGCAGAAATGATGATCAAGACACAAACAGATCCTCCT	24831
Sbjct	2106		ACCTCCAGCATAATGACAGAATCAGCAGAAATGATGATCAAGACACAAACAGATCCTCCT	2047
Query	24832		GGGTCTACACCAGAGAGTACTCATACTGTGGACATATCAACAACACCCAACTGGGTAGAA	24891
Sbjct	2046		GGGTCTACACCAGAGAGTACTCATACTGTGGACATATCAACAACACCCAACTGGGTAGAA	1987
Query	24892		ACCCAC-TCGACT-GTGAC-TCAGAGATTTTCACACTCAGAGATGACCACTCTTGTGAGC	24948
Sbjct	1986		ACCCACTTCGACTNGTGACTTCAGAGATTTTGACACTCAGAGATGACCACTCTTGTGAGC	1927
Query	24949		-AGAAG-CCCTGG-TGAT-ATGTTAT--GGCCTAGTCAATCCTCTGTGGAAGAAACCAGC	25002
Sbjct	1926		TAGAAGCCCCTGGTTGATAATGTTATTGGGCCTAGTCAATCCTCTGTGGAAGAAACCAGC	1867
Query	25003		TCTGCCTCTTCCCTGCTGTCTCTGCCTGCCACGACCTCACCTTC-TCCTGTTTCCTCTAC	25061
Sbjct	1866		TCTGCCTCTTCCCTGCTGTCTCTGCCTGCCACGACCTCACCTTCGTCCTGTTTCCTCTAC	1807
Query	25062		-ATTAGTAGAGG-ATTTCCCTTCCGCTTCTCTTCTGTGACTTCTCTTCTC-ACCCCT-G	25117
Sbjct	1806		AATTAGTAGAGGAATTTCCCTTCCGCTTCTCTTCTGTGACTTCTCTTCTCAACCCCTGG	1747
Query	25118		GCCTGGTGATAACCCACAGACAGGATGGGCATAAGC-AGAGAA-CCTGGAACCAAGTTCCAC	25175
Sbjct	1746		GCCTGGTGATAACCCACAGACAGGATGGGCATAAGCAAGAGAAGCCTGGAACCAAGTTCCAC	1687
Query	25176		TTCAAATTTGAGCAGCACCTCCCATGAGAGACTGACCACT-TTGGAAGACACTGTAGATA	25234
Sbjct	1686		TTCAAATTTGAGCAGCACCTCCCATGAGAGACTGACCACTGTTGGAAGACACTGTAGATA	1627
Query	25235		CAGAAGACATGCAGCCTTCCAC-ACACACAGCAGTGACCAACGTGAGGACCTCCATTCT	25293
Sbjct	1626		CAGAAGACATGCAGCCTTCCACAACACACAGCAGTGACCAACGTGAGGACCTCCATAACT	1567
Query	25294		GGACATGAATCACAATCTTC	25313
Sbjct	1566		GGAGCAGAATCACAATCTTC	1547

Score = 635 bits (330), Expect = 8e-177
 Identities = 355/360 (98%), Gaps = 4/360 (1%)
 Strand=Plus/Plus

Query	15574	AACACAGAAGAGACCAATGTGAAAGCCAACAACCTCTGGACATGAATCCCATTCCCCTGCA	15633
Sbjct	29127	AACACAGAAGAGACCAATGTGAAAGCCAACAACCTCTGGACATGAATCCCATTCCCCTGCA	29186
Query	15634	CTGGCTGACTCAGAGACACCCAAAGCCACAACCTCAAATGGTTATCACCACCACTGTGGGA	15693
Sbjct	29187	CTGGCTGACTCAGAGACACCCAAAGCCACAACCTCAAATGGTTATCACCACCACTGTGGGA	29246
Query	15694	GATCCAGCTCCTTCCACATCAATGCCAGTGCATGGTTCCTCTGAGACTACAAACATTAAG	15753
Sbjct	29247	GATCCAGCTCCTTCCACATCAATGCCAGTGCATGGTTCCTCTGAGACTACAAACATTAAG	29306
Query	15754	AGAGAGCCAACATATTTCTTGACTCCTAG-ACTGAGAGAGACCAGTACCTCTCAGGAGTC	15812
Sbjct	29307	AGAGAGCCAACATATTTCTTGACTCCTAGAACTGAGAGAGACCAGTACCTCTCAGGAGTC	29366
Query	15813	CAGCTTTCCACGGACACAAGTTTTCTACTTTCCAAAGTCCCCACTGGTACTATTACTGA	15872
Sbjct	29367	CAGCTTTCCACGGACACAAGTTTTCTACTTTCCAAAGTCCCCACTGGTACTATTACTGA	29426
Query	15873	GGTCTCCAGTACAGGG-GTCAACTCTTCTAGCAAAATTTCCA--CCCAGACCATGATAA	15929
Sbjct	29427	GGTCTCCAGTACAGGGNGTCATCTCTTCTAGCAAAATTTCCANNCCCCAGACCATGATAA	29486

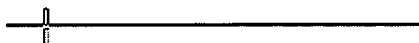
Score = 619 bits (322), Expect = 3e-172
 Identities = 335/339 (98%), Gaps = 2/339 (0%)
 Strand=Plus/Plus

Query	16580	CCACCCTGGGGGACACAAGTGTTTCCACATCAACTCCTAATATCTCTCAGACTAACCAAA	16639
Sbjct	8229	CCACCCTGGGGGACACAAGTGTTTCCACATCAACTCCTAATATCTCTCAGACTAACCAAA	8288
Query	16640	TTCAAACAGAGCCAACAGCATCCCT--GAGCCCTAGACTGAGGGAGAGCAGCACGTCTGA	16697
Sbjct	8289	TTCAAACAGAGCCAACAGCATCCCGTGGAGCCCTAGACTGAGGGAGAGCAGCACGTCTGA	8348
Query	16698	GAAGACCAGCTCAACAACAGAGACAAATACTGCCTTTTCTTATGTGCCACAGGTGCTAT	16757
Sbjct	8349	GAAGACCAGCTCAACAACAGAGACAAATACTGCCTTTTCTTATGTGCCACAGGTGCTAT	8408
Query	16758	TACTCAGGCCTCCAGAACAGAAATCTCCTCTAGCAGAACATCCATCTCAGACCTTGATCG	16817
Sbjct	8409	TACTCAGGCCTCCAGAACAGAAATCTCCTCTAGCAGAACATCCATCTCAGACCTTGATCG	8468
Query	16818	GCCCACAATAGCACCCGACATCTCCACAGGAATGATCACCAGGCTCTTCACCTCCCCCAT	16877
Sbjct	8469	GTCCACAATAGCACCCGACATCTCCACAGGAATGATCACCAGGCTCTTCACCTCCCCCAT	8528
Query	16878	CATGACAAAATCTGCAGAAATGACCGTCACCACTCAAAC	16916
Sbjct	8529	CATGACAAAATCTGCAGAAATGACCGTCACCACTCAAAC	8567

Score = 440 bits (229), Expect = 2e-118

Identities = 245/248 (98%), Gaps = 2/248 (0%)
Strand=Plus/Plus

Query	9858	CCCAGAGATCAGGTCCACTGTGCGAAATTCTCCTTGGGAAGACTCCAGAAACAAGTGTTC	9917
Sbjct	29795	CCCAGAGATCAGGTC-ACTGTGAGAAATTCTCCTTGGGAAGACTCCAGAAACAAGTGTTC	29853
Query	9918	CATGGAGACCACAG-TGGAACCAGTCACCCTTCAGTCCACAGCCCTAGGAAGTGGCAGCA	9976
Sbjct	29854	CATGGAGACCACAGNTGGAACCAGTCACCCTTCAGTCCACAGCCCTAGGAAGTGGCAGCA	29913
Query	9977	CCAGCATCTCTCACCTGCCCACAGGAACCACATCACCAACCAAGTCACCAACAGAAAATA	10036
Sbjct	29914	CCAGCATCTCTCACCTGCCCACAGGAACCACATCACCAACCAAGTCACCAACAGAAAATA	29973
Query	10037	TGTTGGCTACAGAAAGGGTCTCCCTCTCCCCATCCCCACCTGAGGCTTGGACCAACCTTT	10096
Sbjct	29974	TGTTGGCTACAGAAAGGGTCTCCCTCTCCCCATCCCCACCTGAGGCTTGGACCAACCTTT	30033
Query	10097	ATTCTGGA 10104	
Sbjct	30034	ATTCTGGA 30041	



Score = 392 bits (204), Expect = 7e-104
Identities = 245/253 (96%), Gaps = 8/253 (3%)
Strand=Plus/Plus

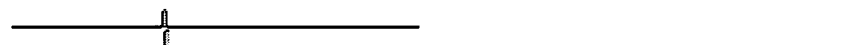
Query	6320	ATTCCACAATCAGTAGGAGGAATGCAATCACTTCCTGGCTATGGGACCTCACTACATCTC	6379
Sbjct	33013	ATTCCACAATCAGTAGGAGGAATGCAATCACTTCCTGGCTATGGGACCTCACTACATCTC	33072
Query	6380	TCCCCACTACAACCTGGCCAAGTACTAGTTTATCTGAGGCACTGTCCTCAGGCCATTCTG	6439
Sbjct	33073	TCCCCACTACAACCTGGCCAAGTACTAGTTTATCTGAGGCACTGTCCTCAGGCCATTCTG	33132
Query	6440	GGGTTTCAAACCCAAGTTCAACTACGACTGAATTTCCACTCTTTTCAGCTGCATCCACAT	6499
Sbjct	33133	GGGTTTCAAACCCAAGTTCAACTACGACTGAATTTCCACTCTTTTCAGCTGCATCCACAT	33192
Query	6500	CTGCTGCTAAGCAA-AGAAATC-CAGAA--ACAGAGACCCATGGTCCC--CAGAATAC--	6551
Sbjct	33193	CTGCTGCTAAGCAACAGAAATCNCAGAANNACAGAGACCCATGGTCCCNNCAGAATACNN	33252
Query	6552	AGCCGCGAGTACT 6564	
Sbjct	33253	AGCCGCGAGTACT 33265	



Score = 369 bits (192), Expect = 6e-97
Identities = 493/636 (77%), Gaps = 5/636 (0%)
Strand=Plus/Plus

Query	24247	ACAGATATGTTGCACAAAAGCTCAGAACCTGTAACCAACTCACCTGCAAATTTGAGCAGC	24306
Sbjct	26182	ACAGACATGTTACACACAAGCCCAGAAC-TGTAACCAG-TCACCTCCAAAGCTGAGCCAC	26239

Query	24307	ACCTCAGTTGAAATACTGGCCACCTCTGAAGTCACCACAGATACAGAGAAAACCTCATCCT	24366
Sbjct	26240	ACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATCCT	26299
Query	24367	TCTTCAAACAGAACAGTGACCGATGTGGGGACCTCCAGTTCTGGACATGAATCCACTTCC	24426
Sbjct	26300	TCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCCCCTTCC	26359
Query	24427	TTTGTCTAGCTGACTCACAGACATCCAAAGTCACATCTCCAATGGTTATTACCTCCACC	24486
Sbjct	26360	TCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCACC	26419
Query	24487	ATGGAGGATACGAGTGTCTCCACATCAACTCCTGGCTTTTTTGAGACTAGCAGAATTTCAG	24546
Sbjct	26420	CAGGAGGATACAACGTGTGCCATATCAACCCCTCACTTCTTGAGACTAGCAGAATTTCAG	26479
Query	24547	ACAGAACCAACATCCTCCCTGACCCTTGGACTGAGAAAGACCAGCAGCTCTGAGGGGACC	24606
Sbjct	26480	AAAGAGTCAATTTCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGACA	26539
Query	24607	AGCTTAGCCACAGAGATGAGCACTGTCTTTCTGGAGTGCCACTGGTGCCACTGCTGAA	24666
Sbjct	26540	AGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCGTTGGTGCTACTACTGAG	26599
Query	24667	GTCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCAGGCTTTGCTCAGCTC	24726
Sbjct	26600	ATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGTCC	26659
Query	24727	ACAGTGTACCAGAGA---CTTCCACAGAAACCATCACCAGACTCCCTACCTCCAGCATA	24783
Sbjct	26660	ACAATGTTGCCAGAAATATCCACCACAAGAAAATCATTAAAGTTCCTACTTCCCCCATC	26719
Query	24784	ATGACAGAATCAGCAGAAATGATGATCAAGACACAAACAGATCCTCCTGGGTCTACACCA	24843
Sbjct	26720	CTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACATCA	26779
Query	24844	GAGAGTACTCATACTGTGGACATATCAACAACACCC	24879
Sbjct	26780	GAGAGTACCTTTACATTAGACACATCAACCACTCCC	26815



Score = 300 bits (156), Expect = 4e-76
 Identities = 440/577 (76%), Gaps = 3/577 (0%)
 Strand=Plus/Plus

Query	25184	TGAGCAGCACCTCCCATGAGAGACTGACCACTTGGGAAGACACTGTAGATACAGAAGACA	25243
Sbjct	26232	TGAGCCACACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTG	26291
Query	25244	TGCAGCCTTCCACACACACAGCAGTGACCAACGTGAGGACCTCCATTTCTGGACATGAAT	25303
Sbjct	26292	TGCATCCTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAAT	26351
Query	25304	CACAATCTTCTGTCTCTATCTGACTCAGAGACACCCAAAGCCACATCTCCAATGGGTACCA	25363
Sbjct	26352	CCCCTTCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTA	26411
Query	25364	CCTACACCATGGGGGAAACGAGTGTTTCCATATCCACTTCTGACTTCTTTGAGACCAGCA	25423
Sbjct	26412	CCTCCACCCAGGAGGATACAACGTGTGCCATATCAACCCCTCACTTCTTGAGACTAGCA	26471

Query	25424	GAATTCAGATAGAACCAACATCCTCCCTGACTTCTGGATTGAGGGAGACCAGCAGCTCTG	25483
Sbjct	26472	GAATTCAGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTG	26531
Query	25484	AGAGGATCAGCTCAGCCACAGAGGGAAGCACTGTCTTTCTGAAGTGCCAGTGGTGCTA	25543
Sbjct	26532	TGGAGACAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGCCGTTGGTGCTA	26591
Query	25544	CCACTGAGGTCTCCAGGACAGAAGTGATATCCTCTAGGGGAACATCCATGTCAGGGCCTG	25603
Sbjct	26592	CTACTGAGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTG	26651
Query	25604	ATCAGTTCACCATATCACCAGACATCTCTA-CTGAAG--CGATCACCAGGCTTTCTACTT	25660
Sbjct	26652	CTGAGTCCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAGTTCCTACTT	26711
Query	25661	CCCCATTATGACAGAATCAGCAGAAAGTGCCATCACTATTGAGACAGGTTCTCCTGGGG	25720
Sbjct	26712	CCCCATCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCTCCTGGGT	26771
Query	25721	CTACATCAGAGGTACCCCTCACCTTGGACACCTCAAC	25757
Sbjct	26772	CTACATCAGAGGTACCTTTACATTAGACACATCAAC	26808

Score = 296 bits (154), Expect = 6e-75
 Identities = 479/634 (75%), Gaps = 5/634 (0%)
 Strand=Plus/Plus

Query	20735	CCACAGACACATTGGGCACAAGCCCAGAACCTACAACCAGTTCACCTCCAAATTTGAGCA	20794
Sbjct	26180	CCACAGACATGTTACACACAAGCCCAGAAC-TGTAACCAGT-CACCTCCAAAGCTGAGCC	26237
Query	20795	GTACCTCACATGTGATACTGACAACAGATGAAGACACCACAGCTATAGAAGCCATGCATC	20854
Sbjct	26238	ACACTTCACATGAGAGACTGACCACTGGCAAGGACACCACAAATACAGAAGCTGTGCATC	26297
Query	20855	CTTCCACAAGCACAGCAGCGACTAATGTGGAAACCACCTGTTCTGGACATGGGTCACAAT	20914
Sbjct	26298	CTTCCACAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCCCCTT	26357
Query	20915	CCTCTGTCTAACTGACTCAGAAAAAACCAAGGCCACAGCTCCAATGGATACCACCTCCA	20974
Sbjct	26358	CCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACCTCCA	26417
Query	20975	CCATGGGGCATACTAAGTGTTCACATCAATGTCTGTTTCTGAGACTACAAAAATTA	21034
Sbjct	26418	CCCAGGAGGATACAACTGTTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGAATTC	26477
Query	21035	AGAGAGAGTCAACATATTCCTTGACTCCTGGACTGAGAGAGACCAGCATTTCCCAAATG	21094
Sbjct	26478	AGAAAGAGTCAATTTCCCTCCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTGGAGA	26537
Query	21095	CCAGCTTTTCCACTGACACAAGTATTGTTCTTTTCAAGTCCCCACTGGTACTACTGCTG	21154
Sbjct	26538	CAAGCTCAGCCATAGAGACAAGTGCTGTCTTTCTGAAGTGTCGTTGGTGCTACTACTG	26597
Query	21155	AGGTCTCCAGGACAGAAGTCACCTCCTCTGGTAGAACATCCATCCCTGGCCCTTCTCAGT	21214
Sbjct	26598	AGATCTCCAGGACAGAAGTCACCTCCTCTAGCAGAACATCCATCTCTGGTTCTGCTGAGT	26657

Query	21215	CCACAGTTTTGCCAGAAATAT---CCACAAGAACAATGACAAGGCTCTTTGCCTCGCCCA	21271
Sbjct	26658	CCACAATGTTGCCAGAAATATCCACCACAAGAAAAATCATTAAGTTCCTACTTCCCCCA	26717
Query	21272	CCATGACAGAATCAGCAGAAATGACCATCCCCACTCAAACAGGTCCTTCTGGGTCTACCT	21331
Sbjct	26718	TCCTGGCAGAATCATCAGAAATGACCATCAAGACCCAAACAAGTCCTCCTGGGTCTACAT	26777
Query	21332	CACAGGATACCCTTACCTTGGACACATCCACCAC	21365
Sbjct	26778	CAGAGAGTACCTTTACATTAGACACATCAACCAC	26811

Score = 291 bits (151), Expect = 3e-73
Identities = 155/157 (98%), Gaps = 0/157 (0%)
Strand=Plus/Minus

Query	17160	AGAGAGCATCCCCTCCTCTCCTCTCCCTGTGACTGCACTTCTTACTTCTGTTCTGGTGAC	17219
Sbjct	8725	AGAGAGCATCCCCTCCTCTCCTCTCCCTGTGACTGCACTTCTTACTTCTGTTCTGGTGAC	8666
Query	17220	AACCACCAATGTATTGGGCACAACAAGCCCAGAGACCGTAACGAGTTCACCTCCAAATTT	17279
Sbjct	8665	AACCACAAATGTATTGGGCACAACAAGCCCAGAGCCCGTAACGAGTTCACCTCCAAATTT	8606
Query	17280	AAGCAGCCCCACACAGGAGAGACTGACCACTTACAAA	17316
Sbjct	8605	AAGCAGCCCCACACAGGAGAGACTGACCACTTACAAA	8569

Score = 266 bits (138), Expect = 1e-65
Identities = 397/524 (75%), Gaps = 3/524 (0%)
Strand=Plus/Plus

Query	22624	CATCCTTTCCCAAACACGGCAGTAACCAAAGTTGGAAGTTCCAGTTCTGGACATGAATCC	22683
Sbjct	26294	CATCCTTCCAAACACAGCAGCGTCCAATGTGGAGATTCCCAGCTCTGGACATGAATCC	26353
Query	22684	CCTTCCTCTGTCTACCTGACTCAGAGACAACCAAAGCCACATCGGCAATGGGTACCATC	22743
Sbjct	26354	CCTTCCTCTGCCTTAGCTGACTCAGAGACATCCAAAGCCACATCACCAATGTTTATTACC	26413
Query	22744	TCCATTATGGGGGATACAAGTGTCTTCTACATTAACCTCCTGCCTTATCTAACACTAGGAAA	22803
Sbjct	26414	TCCACCCAGGAGGATACAAGTGTGCCATATCAACCCCTCACTTCTTGGAGACTAGCAGA	26473
Query	22804	ATTCAGTCAGAGCCAGCTTCTCACTGACCACCAGATTGAGGGAGACCAGCACCTCTGAA	22863
Sbjct	26474	ATTCAGAAAGAGTCAATTTCTCCTGAGCCCTAAATTGAGGGAGACAGGCAGTTCTGTG	26533
Query	22864	GAGACCAGCTTAGCCACAGAAGCAAACACTGTTCTTTCTAAAGTGTCCACTGGTGCTACT	22923
Sbjct	26534	GAGACAAGCTCAGCCATAGAGACAAGTGCTGCTTTCTGAAGTGTCCGTTGGTGCTACT	26593
Query	22924	ACTGAGGTCTCCAGGACAGAAGCCATCTCCTTTAGCAGAACATCCATGTCAGGCCCTGAG	22983